



#3

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SEQUENCE LISTING

<110> ADAMS, DANIEL P.  
SHOPE, ROBERT J.

<120> METHOD AND COMPOSITION FOR ALTERING A T CELL MEDIATED  
PATHOLOGY

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<140> 09/927,122

<141> 2001-08-10

<160> 58

<170> PatentIn Ver. 2.1

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DNA sequence

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| ggtggtgggtg | gaggcgctgg  | aatgttaggc | acgggagaag  | gtggtggcgg | cgggtgccgcc | 5700 |
| ggtataattt  | gttctggttt  | agtttggtcg | cgcacgattg  | tgggcaccgg | cgcaggcgcc  | 5760 |
| gctggctgca  | caacggaagg  | tcgtctgctt | cgaggcagcg  | cttgggggtg | tggcaattca  | 5820 |
| atattataat  | tgggaatacaa | atcgtaaaaa | tctgctataa  | gcattgtaat | ttcgctatcg  | 5880 |
| tttaccgtgc  | cgatatattaa | caaccgctca | atgtaagcaa  | ttgtattgta | aagagattgt  | 5940 |
| ctcaagctcc  | gcacgccgat  | aacaagcctt | ttcattttta  | ctacagcatt | gtagtggcga  | 6000 |
| gacacttcgc  | tgctcgtcgc  | tcgagttcta | tagtgtcacc  | taaatcgat  | gtgtatgata  | 6060 |
| cataagggtta | tgtatttaatt | gtagccgcgt | tctaacgaca  | atatgtccat | atggtgcact  | 6120 |
| ctcagtacaa  | tctgctctga  | tgccgcatag | ttaagccagc  | cccgacaccc | gccaacaccc  | 6180 |
| gctgacgcgc  | cctgacgggc  | ttgtctgctc | ccggcatccg  | cttacagaca | agctgtgacc  | 6240 |
| gtctccggga  | gctgcatgtg  | tcagaggttt | tcaccgtcat  | caccgaaacg | cgcgagagga  | 6300 |
| aagggcctcg  | tgatacgcct  | atttttatag | gttaattgtca | tgataataat | ggtttcttag  | 6360 |
| acgtcagggtg | gcacttttcg  | gggaaatgtg | cgcggaaccc  | ctatttggtt | atttttctaa  | 6420 |
| atacattcaa  | atatgtatcc  | gtcatgaga  | caataaccct  | gataaatgct | tcaataatat  | 6480 |



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| gcattttgcc  | ttcctgtttt | tgctcaccca  | gaaacgctgg  | tgaaagtaaa | agatgctgaa | 6600 |
| gatcagttgg  | gtgcacgagt | gggttacatc  | gaactggatc  | tcaacagcgg | taagatcctt | 6660 |
| gagagttttc  | gccccgaaga | acgtttttcca | atgatgagca  | cttttaaagt | tctgctatgt | 6720 |
| ggcgcggtat  | tatcccgtat | tgacgcgggg  | caagagcaac  | tcggtcgccg | catacactat | 6780 |
| tctcagaatg  | acttggttga | gtactcacca  | gtcacagaaa  | agcatcttac | ggatggcatg | 6840 |
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| cttctgacaa  | cgatcggagg | accgaaggag  | ctaaccgctt  | ttttgcacaa | catgggggat | 6960 |
| catgtaactc  | gccttgatcg | ttgggaaccg  | gagctgaatg  | aagccatacc | aaacgacgag | 7020 |
| cgtgacacca  | cgatgcctgt | agcaatggca  | acaacgttgc  | gcaaactatt | aactggcgaa | 7080 |
| ctacttactc  | tagcttcccc | gcaacaatta  | atagactgga  | tggaggcgga | taaagttgca | 7140 |
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| gcctttgagt  | gagctgatac | cgctcgccgc  | agccgaacga  | ccgagcgag  | cgagtcagtg | 8280 |
| agcgaggaag  | cggaagagcg | cccaatacgc  | aaaccgcctc  | tccccgcgcg | ttggccgatt | 8340 |
| cattaatgca  | ggttaacctg | gcttatcgaa  | attaatacga  | ctcactatag | ggagaccggc | 8400 |
| agatcgatct  | gtcga      |             |             |            |            | 8415 |

&lt;210&gt; 8

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 8

actagttttt atggtcgtgt acatttctta catctatgcg

40

&lt;210&gt; 9

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 9

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28

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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

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<210> 11  
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<220>  
<223> Description of Artificial Sequence: Primer

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<210> 12  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
ctgtgcacct ccttcccatt cac 23

<210> 13  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
ggcagtatct ggagtcattg agg 23

<210> 14  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
gcgacctcgg gtgggcccac cgttgtttca gg 32

<210> 15  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
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<210> 16  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
actagtgcaa cgttgactaa gaatttcattg cggccgc 37

<210> 17  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
gcggccgcat gaaattctta gtcaacggtg cactagt 37

<210> 18  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18  
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<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

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<210> 20

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

tgtgactagt atgtatcggc ccatcggtct tccccct

37

<210> 21

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21

tttctagact attatttacc cggagacagg gagag

35

<210> 22

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 22

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43

<210> 23

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

cccaagcttc tattaacact ctcccctggt gaagct

36

<210> 24

<211> 279

<212> PRT

<213> Unknown Organism

&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: TCR alpha chain

&lt;400&gt; 24

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Met Ala Cys Pro Gly Phe Leu Trp Ala Leu Val Ile Ser Thr Cys Leu
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Glu Phe Ser Met Ala Gln Thr Val Thr Gln Ser Gln Pro Glu Met Ser
      20              25              30

Val Gln Glu Ala Glu Thr Val Thr Leu Ser Cys Thr Tyr Asp Thr Ser
      35              40              45

Glu Ser Asp Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Arg Gln
 50              55              60

Met Ile Leu Val Ile Arg Gln Glu Ala Tyr Lys Gln Gln Asn Ala Thr
 65              70              75              80

Glu Asn Arg Phe Ser Val Asn Phe Gln Lys Ala Ala Lys Ser Phe Ser
      85              90              95

Leu Lys Ile Ser Asp Ser Gln Leu Gly Asp Ala Ala Met Tyr Phe Cys
      100              105              110

Ala Tyr Arg Ser Ala Tyr Ser Gly Ala Gly Ser Tyr Gln Leu Thr Phe
      115              120              125

Gly Lys Gly Thr Lys Leu Ser Val Ile Pro Asn Ile Gln Asn Pro Asp
      130              135              140

Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val
      145              150              155              160

Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys
      165              170              175

Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser
      180              185              190

Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp
      195              200              205

Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr
      210              215              220

Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys
      225              230              235              240

Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile
      245              250              255

Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met
      260              265              270

Thr Leu Arg Leu Trp Ser Ser
      275

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|            |            |           |            |            |            |            |           |            |            |            |            |           |            |            |            |
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| Met<br>1   | Gly        | Thr       | Ser        | Leu<br>5   | Leu        | Cys        | Trp       | Met        | Ala<br>10  | Leu        | Cys        | Leu       | Leu        | Gly<br>15  | Ala        |
| Asp        | His        | Ala       | Asp<br>20  | Thr        | Gly        | Val        | Ser       | Gln<br>25  | Asn        | Pro        | Arg        | His       | Lys<br>30  | Ile        | Thr        |
| Lys        | Arg        | Gly<br>35 | Gln        | Asn        | Val        | Thr        | Phe<br>40 | Arg        | Cys        | Asp        | Pro        | Ile<br>45 | Ser        | Glu        | His        |
| Asn        | Arg<br>50  | Leu       | Tyr        | Trp        | Tyr        | Arg<br>55  | Gln       | Thr        | Leu        | Gly        | Gln<br>60  | Gly       | Pro        | Glu        | Phe        |
| Leu<br>65  | Thr        | Tyr       | Phe        | Gln        | Asn<br>70  | Glu        | Ala       | Gln        | Leu        | Glu<br>75  | Lys        | Ser       | Arg        | Leu        | Leu<br>80  |
| Ser        | Asp        | Arg       | Phe        | Ser<br>85  | Ala        | Glu        | Arg       | Pro        | Lys<br>90  | Gly        | Ser        | Phe       | Ser        | Thr<br>95  | Leu        |
| Glu        | Ile        | Gln       | Arg<br>100 | Thr        | Glu        | Gln        | Gly       | Asp<br>105 | Ser        | Ala        | Met        | Tyr       | Leu<br>110 | Cys        | Ala        |
| Ser        | Ser<br>115 | Pro       | Gly        | Thr        | Ser        | Tyr<br>120 | Glu       | Gln        | Tyr        | Phe        | Gly<br>125 | Pro       | Gly        | Thr        | Arg        |
| Leu<br>130 | Thr        | Val       | Thr        | Glu        | Asp<br>135 | Leu        | Lys       | Asn        | Val        | Phe        | Pro<br>140 | Pro       | Glu        | Val        | Ala        |
| Val<br>145 | Phe        | Glu       | Pro        | Ser        | Glu<br>150 | Ala        | Glu       | Ile        | Ser        | His<br>155 | Thr        | Gln       | Lys        | Ala        | Thr<br>160 |
| Leu        | Val        | Cys       | Leu        | Ala<br>165 | Thr        | Gly        | Phe       | Tyr        | Pro<br>170 | Asp        | His        | Val       | Glu        | Leu<br>175 | Ser        |
| Trp        | Trp        | Val       | Asn<br>180 | Gly        | Lys        | Glu        | Val       | His<br>185 | Ser        | Gly        | Val        | Ser       | Thr<br>190 | Asp        | Pro        |
| Gln        | Pro<br>195 | Leu       | Lys        | Glu        | Gln        | Pro<br>200 | Ala       | Leu        | Asn        | Asp        | Ser<br>205 | Arg       | Tyr        | Cys        | Leu        |
| Ser<br>210 | Ser        | Arg       | Leu        | Arg        | Val        | Ser<br>215 | Ala       | Thr        | Phe        | Trp        | Gln<br>220 | Asn       | Pro        | Arg        | Asn        |
| His<br>225 | Phe        | Arg       | Cys        | Gln        | Val<br>230 | Gln        | Phe       | Tyr        | Gly        | Leu<br>235 | Ser        | Glu       | Asn        | Asp        | Glu<br>240 |
| Trp        | Thr        | Gln       | Asp        | Arg<br>245 | Ala        | Lys        | Pro       | Val        | Thr<br>250 | Gln        | Ile        | Val       | Ser        | Ala<br>255 | Glu        |

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln  
                   260                                  265                                  270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala  
                   275                                  280                                  285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val  
                   290                                  295                                  300

Lys Arg Lys Asp Ser Arg Gly  
 305                                  310

<210> 26  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 26  
 aaatgataac catctcgc 18

<210> 27  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 27  
 tttactgttt tcgtaacagt ttg 24

<210> 28  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 28  
 ttggagggcg ttatccacct tc 22

<210> 29  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 29  
 ctgtaaatca acaacgcaca g 21

<210> 30  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 30  
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<210> 31  
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 <223> Description of Artificial Sequence: Primer

<400> 31  
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<210> 32  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 32  
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<210> 33  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 33  
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<210> 34  
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<220>



<223> Description of Artificial Sequence: Primer

<400> 34

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22

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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23

<210> 36

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 36

ggtcgttaac aatggggaag ctg

23

<210> 37

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37

tttactgttt tcgtaacagt ttg

24

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 38

ggtcgttaac aatggggaag ctg

23

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 39

gaagtcactt atgagacaca ccag

24

&lt;210&gt; 40

&lt;400&gt; 40

000

&lt;210&gt; 41

&lt;211&gt; 9182

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Plasmid pTRABac/9F12  
DNA sequence

&lt;400&gt; 41

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| cccagcatgc  | ctgctattgt  | cttcccaatc | ctcccccttg  | ctgtcctgcc  | ccaccccacc  | 2160 |
| ccccagaata  | gaatgacacc  | tactcagaca | atgcatgca   | atttcctcat  | tttattagga  | 2220 |
| aaggacagtg  | ggagtggcac  | cttccagggg | caaggaaggc  | acgggggagg  | ggcaaacaac  | 2280 |
| agatggctgg  | caactagaag  | gcacagtcga | ggctgatcag  | cgagctctag  | tctagactat  | 2340 |
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| cgtctaaagg | tgcagcgggt  | tgagggttcg | tcggcattgg  | tgagcggggc  | ggcaattcag  | 5640 |
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| gcggcggtgc | cgccggtata  | atttgttctg | gttttagttt  | ttcgcgacag  | attgtgggca  | 5760 |
| ccggcgagag | cgccgctggc  | tgcaacaacg | aaggctcgtc  | gcttcgaggc  | agcgcttggg  | 5820 |
| gtggtggcaa | ttcaatatta  | taattggaat | acaaatcgta  | aaaatctgct  | ataagcattg  | 5880 |
| taatttcgct | atcgtttacc  | gtgccgat   | ttaacaacgc  | ctcaatgtaa  | gcaattgtat  | 5940 |
| tgtaaagaga | ttgtctcaag  | ctccgcacgc | cgataacaag  | ccttttcatt  | tttactacag  | 6000 |
| cattgtagt  | gcgagacact  | tcgctgtcgt | cgactcgagt  | tctatagtgt  | cacctaaattc | 6060 |
| gtatgtgtat | gatacataag  | gttatgtatt | aattgtagcc  | gcgttctaac  | gacaatatgt  | 6120 |
| ccatatggtg | cactctcagt  | acaatctgct | ctgatgccgc  | atagttaagc  | cagccccgac  | 6180 |
| acccgccaac | acccgctgac  | gcgccctgac | gggcttgtct  | gctcccggca  | tccgcttaca  | 6240 |
| gacaagctgt | gaccgtctcc  | gggagctgca | tgtgtcagag  | gttttcaccg  | tcatacccca  | 6300 |
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| ttcccttttt | tgccgcat    | tgcccttctg | tttttgccta  | cccagaaaacg | ctggtgaaa   | 6600 |
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| gcggtaaag  | ccttgagagt  | tttcgccccg | aagaacgttt  | tccaatgatg  | agcactttta  | 6720 |
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| acaacatggg | ggatcatgta  | actcgcttgc | atcggtggga  | accggagctg  | aatgaagcca  | 7020 |
| taccaaacga | cgagcgtgac  | accacgatgc | ctgtagcaat  | ggcaacaacg  | ttgcgcaaac  | 7080 |
| tattaaactg | cgaactactt  | actctagctt | cccgcgaaca  | attaatagac  | tggatggagg  | 7140 |
| cggataaagt | tgcaggacca  | cttctgcgct | cggcccttcc  | ggctgggtgg  | tttattgctg  | 7200 |
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 agctgtgtat ctgtgtgccg gcagtaccgg gacagaaacg ctgtattttg gtcaggaac 360  
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